

Ramsey
RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 09/598,982C

Source: 1FW16

Date Processed by STIC: 8/10/05

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**CRF Errors Edited by the STIC Systems
Branch**

Serial Number: 09/598,982C

CRF Edit Date: 8/10/05
Edited by: 182

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:

converted submitted file to a generated
Patent In sequence listing

Revised 09/09/2003



IFW16

RAW SEQUENCE LISTING

DATE: 08/10/2005

PATENT APPLICATION: US/09/598,982C

TIME: 10:50:00

Input Set : A:\34506104.ST25.txt

Output Set: N:\CRF4\08102005\I598982C.raw

3 <110> APPLICANT: Niles, Andrew
 4 Maffitt, Mark
 5 Haak-Frendscho, Mary
 7 <120> TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TRYPTASES, ACTIVE SITE MUTANTS
 THEREOF,
 8 AND METHODS OF MAKING SAME
 10 <130> FILE REFERENCE: 34506.104
 12 <140> CURRENT APPLICATION NUMBER: 09/598,982C
 13 <141> CURRENT FILING DATE: 2000-06-21
 15 <150> PRIOR APPLICATION NUMBER: 09/079,970
 16 <151> PRIOR FILING DATE: 1998-04-15
 18 <160> NUMBER OF SEQ ID NOS: 52
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 735
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(735)
 32 <400> SEQUENCE: 1
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 34 ile val gly gly gln glu ala pro arg ser lys trp pro trp gln val
 35 1 5 10 15
 37 agc ctg aga gtc cac ggc cca tac tgg atg cac ttc tgc ggg ggc tcc 96
 38 ser leu arg val his gly pro tyr trp met his phe cys gly gly ser
 39 20 25 30
 41 ctc atc cac ccc cag tgg gtg ctg acc gca gcg cac tgc gtg gga ccg 144
 42 leu ile his pro gln trp val leu thr ala ala his cys val gly pro
 43 35 40 45
 45 gac gtc aag gat ctg gcc gcc ctc agg gtg caa ctg cgg gag cag cac 192
 46 asp val lys asp leu ala ala leu arg val gln leu arg glu gln his
 47 50 55 60
 49 ctc tac tac cag gac cag ctg ctg ccg gtc agc agg atc atc gtg cac 240
 50 leu tyr tyr gln asp gln leu leu pro val ser arg ile ile val his
 51 65 70 75 80
 53 cca cag ttc tac acc gcc cag atc gga gcg gac atc gcc ctg ctg gag 288
 54 pro gln phe tyr thr ala gln ile gly ala asp ile ala leu leu glu
 55 85 90 95
 57 ctg gag gag ccg gtg aac gtc tcc agc cac gtc cac acg gtc acc ctg 336
 58 leu glu glu pro val asn val ser ser his val his thr val thr leu
 59 100 105 110
 61 ccc cct gcc tca gag acc ttc ccc ccg ggg atg ccg tgc tgg gtc act 384
 62 pro pro ala ser glu thr phe pro pro gly met pro cys trp val thr

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63      115      120      125
65 ggc tgg ggc gat gtg gac aat gat gag cgc ctc cca ccg cca ttt cct 432
66 Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro
67      130      135      140
69 ctg aag cag gtg aag gtc ccc ata atg gaa aac cac att tgt gac gca 480
70 Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala
71 145      150      155      160
73 aaa tac cac ctt ggc gcc tac acg gga gac gac gtc cgc atc gtc cgt 528
74 Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
75      165      170      175
77 gac gac atg ctg tgt gcc ggg aac acc cgg agg gac tca tgc cag ggc 576
78 Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly
79      180      185      190
81 gac tcc gga ggg ccc ctg gtg tgc aag gtg aat ggc acc tgg ctg cag 624
82 Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
83      195      200      205
85 gcg ggc gtg gtc agc tgg ggc gag ggc tgt gcc cag ccc aac cgg cct 672
86 Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
87      210      215      220
89 ggc atc tac acc cgt gtc acc tac tac ttg gac tgg atc cac cac tat 720
90 Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr
91 225      230      235      240
93 gtc ccc aaa aag ccg 735
94 Val Pro Lys Lys Pro
95      245
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 245
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 2
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106 1      5      10      15
109 Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser
110      20      25      30
113 Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro
114      35      40      45
117 Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His
118      50      55      60
121 Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His
122 65      70      75      80
125 Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu
126      85      90      95
129 Leu Glu Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu
130      100      105      110
133 Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr
134      115      120      125
137 Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro
138      130      135      140
141 Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala

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142-145      150      155      160
145 Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
146      165      170      175
149 Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly
150      180      185      190
153 Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
154      195      200      205
157 Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
158      210      215      220
161 Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr
162 225      230      235      240
165 Val Pro Lys Lys Pro
166      245
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170 <211> LENGTH: 40
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: PCR primer
177 <400> SEQUENCE: 3
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181 <210> SEQ ID NO: 4
182 <211> LENGTH: 40
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: PCR primer
189 <400> SEQUENCE: 4
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194 <211> LENGTH: 771
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (7)..(753)
203 <400> SEQUENCE: 5
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205      Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser
206      1      5      10
208 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg
209 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
210 15      20      25      30
212 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca
213 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
214      35      40      45
216 gcg cac tgc gtg gga ccg gac gtc aag gat ctg gcc gcc ctc agg gtg
217 Ala His Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val
218      50      55      60

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144

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220  caa ctg cgg gag cag cac ctg tac tac cag gac cag ctg ctg ccg gtc      240
221  Gln Leu Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val
222      65                      70                      75
224  agc agg atc atc gtg cac cca cag ttc tac acc gcc cag atc gga gcg      288
225  Ser Arg Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala
226      80                      85                      90
228  gac atc gcc ctg ctg gag ctg gag gag ccg gtg aac gtc tcc agc cac      336
229  Asp Ile Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His
230  95                      100                      105                      110
232  gtc cac acg gtc acc ctg ccc cct gcc tca gag acc ttc ccc ccg ggg      384
233  Val His Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly
234      115                      120                      125
236  atg ccg tgc tgg gtc act ggc tgg ggc gat gtg gac aat gat gag cgc      432
237  Met Pro Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg
238      130                      135                      140
240  ctg cca ccg cca ttt cct ctg aag cag gtg aag gtc ccc ata atg gaa      480
241  Leu Pro Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu
242      145                      150                      155
244  aac cac att tgt gac gca aaa tac cac ctt ggc gcc tac acg gga gac      528
245  Asn His Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp
246      160                      165                      170
248  gac gtc cgc atc gtc cgt gac gac atg ctg tgt gcc ggg aac acc ccg      576
249  Asp Val Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg
250  175                      180                      185                      190
252  agg gac tca tgc cag ggc gac tcc gga ggg ccc ctg gtg tgc aag gtg      624
253  Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val
254      195                      200                      205
256  aat ggc acc tgg ctg cag gcg ggc gtg gtc agc tgg ggc gag ggc tgt      672
257  Asn Gly Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys
258      210                      215                      220
260  gcc cag ccc aac ccg cct ggc atc tac acc cgt gtc acc tac tac ttg      720
261  Ala Gln Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu
262      225                      230                      235
264  gac tgg atc cac cac tat gtc ccc aaa aag ccg tgaagcggcc gccgtcgt      771
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266      240                      245
269  <210> SEQ ID NO: 6
270  <211> LENGTH: 249
271  <212> TYPE: PRT
272  <213> ORGANISM: Homo sapiens
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276  Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp
277  1                      5                      10                      15
280  Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe
281      20                      25                      30
284  Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His
285      35                      40                      45
288  Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu
289      50                      55                      60

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292 Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg
293 65 70 75 80
296 Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile
297 85 90 95
300 Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His Val His
301 100 105 110
304 Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro
305 115 120 125
308 Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro
309 130 135 140
312 Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His
313 145 150 155 160
316 Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val
317 165 170 175
320 Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp
321 180 185 190
324 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly
325 195 200 205
328 Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln
329 210 215 220
332 Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp
333 225 230 235 240
336 Ile His His Tyr Val Pro Lys Lys Pro
337 245
340 <210> SEQ ID NO: 7
341 <211> LENGTH: 27
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Mutagenesis oligonucleotide
348 <400> SEQUENCE: 7
349 gaggagccgg tgaaggtctc cagccac 27
352 <210> SEQ ID NO: 8
353 <211> LENGTH: 771
354 <212> TYPE: DNA
355 <213> ORGANISM: Homo sapiens
358 <220> FEATURE:
359 <221> NAME/KEY: CDS
360 <222> LOCATION: (7)..(753)
362 <400> SEQUENCE: 8
363 gggccc ctc gag aaa aga atc gtc ggg ggt cag gag gcc ccc agg agc 48
364 Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser
365 1 5 10
367 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg 96
368 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
369 15 20 25 30
371 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca 144
372 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
373 35 40 45

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VERIFICATION SUMMARY

DATE: 08/10/2005

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